Name: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Date: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Period: \_\_\_\_\_\_\_\_

**Hardy Weinberg Equilibrium Simulation**

Mrs. Krouse, AP Biology, 2015-2016

**Directions:** Working in groups, you will test Hardy Weinberg Equilibrium in a population by tracking the inheritance of one trait—eye color in humans. We will assume that there are two alleles for eye color, brown and blue. We will use “A” to represent the brown allele and “a” to represent the blue allele because the brown allele is dominant. We will be using two different bead colors to represent the different alleles. Because I could not find brown beads, we will use black beads to represent the brown allele. We will use blue beads to represent the blue allele.

Remember, each individual has two alleles for a particular trait, which comprise his/her genotype. The following genotypes result in the following phenotypes (eye colors).

|  |  |  |  |
| --- | --- | --- | --- |
| **Allele Descriptions** | **Bead Representations** | **Genotype** | **Eye Color** |
| Two brown alleles (A and A) | Two black beads | AA | Brown Eyes |
| One brown allele (A) and one blue allele (a) | One black bead and one blue bead | Aa | Brown Eyes |
| Two blue alleles (a and a) | Two blue beads | aa | Blue Eyes |

You and your group members will be given a bag containing 100 beads to represent the alleles present in the gene pool of the population of humans in generation 1. 50 of these beads will be black (to represent the brown alleles in the gene pool) and 50 will be blue (to represent the blue alleles in the gene pool). Because each person in the population receives 2 alleles, you can assume that there are 50 individuals in the population.

Based on this information, what are the allele frequencies in generation 1? Remember, allele frequencies are decimal frequencies, so you will need to take the number of beads that represent a particular allele and divide it by the total number of beads (i.e. the total number of alleles in the population).

**Allele Frequencies in Generation 1:**

A (brown allele) frequency = p = \_\_\_\_\_\_\_\_\_\_

a (blue allele) frequency = q = \_\_\_\_\_\_\_\_\_\_

If the population is in Hardy Weinberg Equilibrium, these allele frequencies should stay the same in the next generation. You should also be able to predict the genotype frequencies (i.e. the frequency of AA, Aa, aa) in the generation 2 using p2, 2pq, and q2.

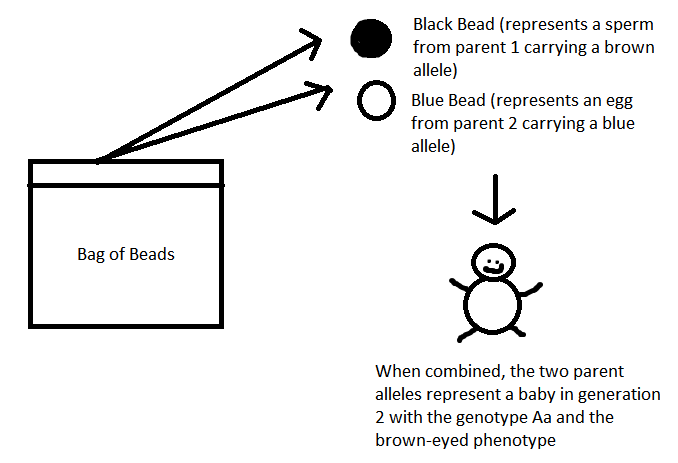
Based on your calculated p and q frequencies, determine the EXPECTED frequencies for each genotype in generation 2 in the chart below. You can also predict the number of individuals with each genotype in generation 2 by taking your calculated decimal frequency and multiplying by 50 (the population size).

**Expected Genotype Frequencies in Generation 2** (assuming allele frequencies do not change from generation 1 to generation 2 because the population is in Hardy Weinberg Equilibrium)

|  |  |  |
| --- | --- | --- |
| **Genotype** | **Decimal Frequency of Genotype** | **# of Individuals with this Genotype in Generation 2** |
| AA | p2 = | p2 x 50 = |
| Aa | 2pq = | 2pq x 50= |
| aa | q2 = | q2 x 50 = |

We are going to run a simulation to see if the allele and genotype frequencies we get in generation 2 when we model reproduction of generation 1 match with our expected frequencies based on Hardy Weinberg Equilibrium. In order to get our observed (i.e. simulation) frequencies, we will follow the procedure given below.

1. Without looking, remove two beads from the bag. These two beads represent the genotype of one individual in the next generation. For example, let’s say you remove one black bead and one blue bead. This individual in generation 2 would have a genotype of Aa. Removing two beads from the bag represents two parents from the generation 1 each contributing one allele carried in reproductive cell (i.e. sperm or egg). These reproductive cells will join together to create a baby in generation 2 with two alleles in its genotype. See image below for clarification.
2. Place a tally mark in the corresponding genotype row in the chart below to represent a baby in generation 2 with this genotype.
3. Put the two beads BACK IN THE BAG and repeat steps 1 and 2 to create another baby.
4. Repeat this procedure until you have 50 tally marks to represent the 50 babies in generation 2.



**Observed Number of Babies with Each Genotype in Generation 2:**

|  |  |  |
| --- | --- | --- |
| **Genotype** | **Tally** | **Number of Babies (count your tally marks)** |
| AA |  |  |
| Aa |  |  |
| aa |  |  |

Use the information in the chart above to determine the genotype frequencies in generation 2. To get a decimal frequency for each genotype, take the number of individuals with this genotype (i.e. the number of tally marks) and divide by the total population size, which is 50 individuals.

**Observed Genotype Frequencies in Generation 2:**

|  |  |  |
| --- | --- | --- |
| **Genotype** | **Number of Babies with this Genotype** | **Decimal Frequency of Genotype** |
| AA |  | p2 = |
| Aa |  | 2pq = |
| aa |  | q2 = |

**Follow-Up Questions:**

1. How do the expected genotype frequencies in generation 2 that you calculated based on Hardy Weinberg Equilibrium compare to the observed genotype frequencies based on the simulation?
2. Does this population appear to be in Hardy Weinberg Equilibrium? Why or why not?